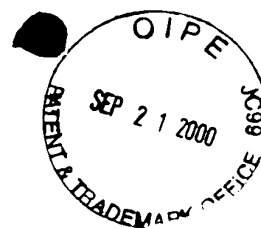


SEQUENCE LISTING



<110> REFF, MITCHELL E.
KLOETZER, WILLIAM S.
NAKAMURA, TAKEHIKO

<120> GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
THEREOF AS THERAPEUTICS

<130> 23522.0699

<140> 09/292,053

<141> 1999-04-14

<150> 08/803,085

<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

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<211> 390

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<213> Homo sapiens

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<222> (1)..(58)

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tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct	96
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser	
-1 1 5 10	

cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt	144
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val	
15 20 25	

ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc	192
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala	
30 35 40 45	

ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct	240
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser	
50 55 60	

gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc 288
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
 65 70 75

tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat 336
 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
 80 85 90

aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc 384
 Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
 95 100 105

cta ggt
 Leu Gly 390
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 -1 1 5 10

Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
 15 20 25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
 30 35 40 45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
 50 55 60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
 65 70 75

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
 80 85 90

Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
 95 100 105

Leu Gly
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<400> 3

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 -15 -10 -5

gtc ctg tcc cag ctg cag ctg cag gag tcg ggc cca gga gtg gtg aag 96
 Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
 -1 1 5 10

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tct gtc 144
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
 15 20 25

agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga 192
 Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
 30 35 40 45

ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac 240
 Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
 50 55 60

aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag 288
 Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
 65 70 75

aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc 336
 Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
 80 85 90

gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta 384
 Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
 95 100 105

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 423
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 110 115 120

<210> 4
 <211> 141
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 -15 -10 -5

Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
15 20 25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
95 100 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
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<210> 5

<211> 387

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<222> (1) . . (387)

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-20 -15 -10

ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc 96
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
-5 -1 1 5 10

ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt 144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
15 20 25

cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa 192
 Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 30 35 40

gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc 240
 Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
 45 50 55

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
 60 65 70

gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag 336
 Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
 75 80 85 90

gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc 384
 Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 95 100 105

aaa 387
 Lys

<210> 6
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 <213> Homo sapiens

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 -20 -15 -10

Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 -5 -1 1 5 10

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 15 20 25

Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 30 35 40

Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
 45 50 55

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
 60 65 70

Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
 75 80 85 90

Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 95 100 105

Lys

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 -15 -10 -5

gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag 96
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
 -1 1 5 10

cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc 144
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
 15 20 25

acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag 192
 Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
 30 35 40 45

ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg 240
 Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
 50 55 60

tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc 288
 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
 65 70 75

aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg 336
 Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 80 85 90

gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc 384
 Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
 95 100 105

cag gga gtc ctg gtc acc gtc tcc tca 411
 Gln Gly Val Leu Val Thr Val Ser Ser
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<210> 8
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 <213> Homo sapiens

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 -1 1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
 15 20 25
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
 30 35 40 45
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
 50 55 60
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
 65 70 75
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 80 85 90
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 95 100 105
Gln Gly Val Leu Val Thr Val Ser Ser
110 115

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<220>
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<210> 10
<211> 35
<212> DNA
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<220>
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<400> 10
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<210> 11
<211> 35
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<213> Artificial Sequence

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35

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 12

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38

<210> 13

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 13

ggtgcagcca ccgtagcttt gatytccasc tt

32

<210> 14

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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34

<210> 15

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 15

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34

<210> 16

<211> 35
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 <400> 16
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 <210> 17
 <211> 21
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 <400> 17
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 <400> 18
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 <210> 19
 <211> 30
 <212> DNA
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 <210> 20
 <211> 33
 <212> DNA
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 <220>
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<210> 21
 <211> 33
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33

<210> 22
 <211> 33
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33

<210> 23
 <211> 46
 <212> DNA
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46

<210> 24
 <211> 31
 <212> DNA
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<400> 24
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<210> 25
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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 <212> DNA
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<400> 27
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<210> 28
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<400> 28
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<210> 31
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<210> 32
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<210> 33
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<223> Description of Artificial Sequence: Primer

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<210> 34
<211> 20
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<210> 35
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<220>

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<211> 30

<212> DNA

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<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

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27

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

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<400> 38

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27

<210> 39

<211> 27

<212> DNA

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<223> Description of Artificial Sequence: Primer

<400> 39

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27